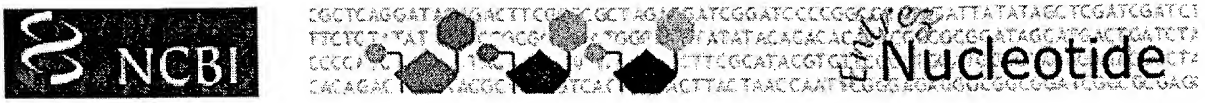
21



1: Z81449. Caenorhabditis el...[gi:1658303]

LOCUS CEC46F11 34841 bp DNA linear INV 02-SEP-1999
DEFINITION Caenorhabditis elegans cosmid C46F11, complete sequence.
ACCESSION Z81449
VERSION Z81449.1 GI:1658303
KEYWORDS HTG; ATP-dependent RNA helicase; Pyridine nucleotide-disulphide oxidoreductases class-I; unc-93.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 34841)
AUTHORS Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M., Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J., Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A., Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M., Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N., Latreille,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B., O'Callaghan,M., Parsons,J., Percy,C., Rifken,L., Roopra,A., Saunders,D., Shownkeen,R., Smaldon,N., Smith,A., Sonnhammer,E., Staden,R., Sulston,J., Thierry-Mieg,J., Thomas,K., Vaudin,M., Vaughan,K., Waterston,R., Watson,A., Weinstock,L., Wilkinson-Sproat,J. and Wohldman,P.
TITLE 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans
JOURNAL Nature 368 (6466), 32-38 (1994)
MEDLINE 94150718
REFERENCE 2 (bases 1 to 34841)
AUTHORS Burton,J.
TITLE Direct Submission
JOURNAL Submitted (04-NOV-1996) Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu
COMMENT Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other available information.
For a graphical representation of this sequence and its analysis see:-
http://webace.sanger.ac.uk/cgi-bin/display?db=wormace&class=Sequence &object=C46F11
Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.
IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.
IMPORTANT: This sequence is not the entire insert of clone C46F11. It may be shorter because we only sequence overlapping sections

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            once, or longer because we arrange for a small overlap between
            neighbouring submissions.
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            sequence Z48241.
            The true right end of clone C46F11 is at 8174 in
            sequence Z48245.
            The start of this sequence (1..102) overlaps with the end of
            sequence Z48241.
            The end of this sequence (34740..34841) overlaps with the start of
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31081 aaaactagca taacttttta aaaatgtcat ctaacaattt ttttaatatt ttttctgta
31141 agaaaaacat tgaaaaatac atagttttgg tcacttttca gttgtattgg ctaagaatca
31201 agtaagatat ttcaatttaa attcgaaaat tgcagtaggt caactctccc cgaccagaaa
31261 tggttaggtt tgtggaaagt gacataactt tgtagatgcg tcatctaaaa aatttttaa
31321 tgtattttat aaaagaaaaa catttaacga tattgttggt aagttttcaa ataaattggt
31381 taaaaattga gtgagacatt ctagtttaaa ttcgagtaat atccgctttc cactgcaaaa
31441 gattaactaa ttgaattttc caatattttc taagattatg aaataatttg taaaatatct
31501 taataaccac attttgtaaa tatgaaataa aaaagtttca acaaaaaaat cgataaaaac
31561 tttttttttc gaatttttcg aaaatttaaa ctctaacaat aaactcgggt atttttagc
31621 tttaaaaatt atttttgga atcaaatcta cgaaattatt caaattagcg taaaaattct
31681 gctcaccaat cagcggcgtt gcccacgccc ctgggcaacg ctttaactct ttttactcat
31741 tttggcactt ttttgagaca ttttttgaag attggcttta cgtaaagtaa tttcacatca
31801 acatttttg tattgcctac tgccaaatat tgtaggcacg taggcaggca cacatgccgg
31861 caaataggca tgctccaatt aaagatcact cctctccaaa tattatgggt attggtgtct
31921 agagagcaac aacaaaaaat gggaagcata aagcaattca aagattcctc ctttttttct
31981 tttctcgcac gcgatagatg tttggcaaaa gaaatgacgc gtggctttcg atatctgaaa
32041 aaataatatt caaaaaaaaa aaatattttt gttgaaaagc tgatgagaaa aagaagaaaa
32101 ggaaataaaa ggtgataata ggaaaaagag gaacaaatga atgatgtgaa gaccggagaa
32161 ggaggcgggt tatcaggtta ttatcacata caaataagcc atattatcag tcaggaggag
32221 cggtatatgg gaacattgct atttgggaaa aagataatag ggcaattatt caaattatga
32281 ataggggaac aaaaggtttg aaccgaccat tgagatgggg ttggagaaca ttttttcaat
32341 tttagcggaa aattcaaatt ttaattacaa aaacacatac ctacttagag ggaaattcaa
32401 ctttttttaat tttttgaaaa ttaatgacaa aattgcatgg gtttttgttt ttcaaaatat
32461 agtattacgg aactatgaga tcatgagaat acctactctt tgccacatgg cctctcgctg
32521 ccgcggcctg ccaatatttt cgcgccagtg aataggcatt ctcatgatct catggtcccg
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33121 ctcaaactga aagtttttc aagtaaaatt ttaaaaaatc aaaattttgg aaggagctat
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33361 gaaaatagaa tattcgtaat tctaaagtct atttggatat agtgaatggc tgaattcggg
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33481 ttcttttctc tttctaatgc aggtcaatca gtgaagacag agagagatag gcgtatagga
33541 aagaagaaag aagaaggagg aaaagggaat tggcaaagaa aaggcataac aataacaaca
33601 gaaagattca acgtcgtcac aaattgaatt gggaacgaac aacaccaaga aacaatcccg
33661 tacacttttt ccagaaatgg aacttttttac agaaacattg aaaaaaaaac cacatgattt
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33781 gctggaaata atcaaaaatt cactttctgg ttcctttttc gcctcccctt tccttctcaa
33841 atgaatcata ttgcaaagta aaagtgagac agaaacattg aattatttat gaaaaaattt
33901 ggtgggtttc atgtgacttt tagattttaa agtaattaaa aattaacatt ttcgttttta
33961 caattccttg atttagttgg ttttggttta cattaaaaat tgttaactaa taaattacag
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34081 caccccgggg gcctcaactt tggaaactta tatctcagtt gttttcaatt atattaaaac
34141 catgttaact acgtgttaat atgtattcta tcgttttcta tatttttgta tttagttgga
34201 catttttga tatcgactag aacaatttag ttaaacactg tcgtcaaagt tgatcctaac
34261 ttcaacttt tggaaaaaaa gtctaactgt atttttaaa caatttttc tttccttaca
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    34321 aaaaagtaat aaaatgaaat tttcagaaaa atatttgaaa ttctcgaaag cagactaaat
    34381 tttgcagaac tttacaacaa atttcgcgga aaaaacccag agacctagca ctttctaaca
    34441 gtgaaaaaat caattcaaga aaataaaatg cttcttttca aaaagtacac aaaactgtac
    34501 gacaccaaat gaggcaagaa tgaaagcatt gctgtccgcc tgcgacaaaa aagtttcaac
    34561 gttcttttct gtcttggtca gggaacgggc ttacatcggt tgacaatgcg attgttccga
    34621 caaaagagaa aaagaagaag aaaaaacatt gaaatggagg ataagttttg gggtttttgt
    34681 tgggaggaat caatttgctt cgaaatctca aagtttcggg aaatttctaa tatttttaa
    34741 tgcaaaattt tggctgaaat tcgggggttt gagggttttt tttaatgaaa aaaatagcat
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22

1: X81823. D.discoideum Hel2...[gi:550328]

Links

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LOCUS       DDHEL2A                 1748 bp    mRNA    linear   INV 02-AUG-1995
DEFINITION  D.discoideum Hel2A mRNA for RNA helicase.
ACCESSION   X81823
VERSION     X81823.1  GI:550328
KEYWORDS    DEAD box protein; Hel2A gene; RNA helicase.
SOURCE      Dictyostelium discoideum
  ORGANISM  Dictyostelium discoideum
            Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE   1
  AUTHORS   Mahal,B. and Nellen,W.
  TITLE     Developmental regulation of DEAD box proteins and cloning of
            putative RNA helicase genes from Dictyostelium discoideum
  JOURNAL   Biol. Chem. Hoppe-Seyler 375 (11), 759-763 (1994)
  MEDLINE   95209781
   PUBMED   7695838
REFERENCE   2  (bases 1 to 1748)
  AUTHORS   Mahal,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-SEP-1994) B. Mahal, Max-Plank Inst.f.Biochemie, Abt.
            Zellbiologie, Am Klopferspitz, 85152 Martinsried b. Munchen, FRG
FEATURES             Location/Qualifiers
     source          1..1748
                     /organism="Dictyostelium discoideum"
                     /mol_type="mRNA"
                     /strain="AX2"
                     /sub_strain="214"
                     /db_xref="taxon:44689"
     gene            1..1748
                     /gene="Hel2A"
     CDS             <1..>1748
                     /gene="Hel2A"
                     /codon_start=3
                     /product="putative RNA helicase"
                     /protein_id="CAA57417.1"
                     /db_xref="GI:550329"
                     /db_xref="GOA:Q23909"
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                     /translation="IPDFRSELGVKITGKDCPKPIQSWAQAGLTEKVHLLLKKFQYEK
                     PTSIQAQTIPAIMNGRDLIGIARTGSGKTLAFLLPMFRHILAQPKSAPGEGMIALIMS
                     PTRELALQIHVECKKFSKVLGLRTACVYGGASISEQIAELKRGADIVVCTPGRMIDIL
                     CANNRRITNLRRVTFLVLDEADRMFDMGFGPQINCIVDSIRPDRQTIMFSATFPPKVE
                     NVAKKILNKPLEIIAGGRSIVSSDIEQFVEVRPTETRFRRLIELLSIWYHKGQILIFT
                     NRQETTDNLYRQLSNSQYQCLSLHGSKDQTDRDETISDFKNKVKTILIATPLASRGLD
                     IKDLNLVVNFDCPDHLEDYVHRVGRTGRAGNRGTAYTFITPDEERFSSSIIKALEQSG
                     SKVPDELRKLNDTYEKKRKEGKDVLLAPTGFTGRGHKFDAAEEDKKNIERKQQRKAYG
                     IEEEEEEEDEDKEKAEKEKLAAASAEKEKQLLSEKEKLDPATTNTIVIPGVDGTIITP
                     SSLLQTDPSVPVGQQAINQIFGISQVTSSEEAIKKLQLAAQLGMKGNIQKLNNQITPL
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     misc_feature    537..548
                     /gene="Hel2A"
                     /note="DEAD-box"
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 121 ttcaatatga aaaaccaaca tcaattcaag cacaaactat acctgcaatt atgaatggtc
 181 gtgatttaat tggtattgcc agaactggtt ccggtaaaac attggcattc cttttaccaa
 241 tgtttcgtca tatactggca caaccaaaat ctgcacctgg tgaaggtatg attgcattga
 301 ttatgtcacc aactagagaa ttggcacttc aaattcatgt tgaatgtaaa aagttttcaa
 361 aagtacttgg attacgtacc gcttgtgttt atggtggtgc aagtataagt gaacaaatag
 421 ccgaattgaa aagaggtgcc gatattgtcg tttgcacacc aggtcgtatg atcgatattt
 481 tatgtgcaaa taatcgacgt atcaccaacc taagacgtgt aacattcttg gtgttggatg
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 721 catcagatat tgaacaattt gtagaggtac gtccaactga aactagattt agacgtttaa
 781 tagaattgct atcgatttgg tatcataaag gtcagatttt aatctttacc aatcgtcaag
 841 agaccaccga caatctatat cgtcaacttt caaactctca atatcaatgt ctatcattac
 901 atggtagtaa agatcaaacc gatcgtgatg aaaccattag tgactttaaa aataaggtta
 961 aaaccatttt aatcgctaca ccattggcat cacgtggttt ggatatcaaa gatttaaatc
1021 ttgtggttaa tttcgattgc cctgatcatt tggaagatta tgttcatagg gtaggtagaa
1081 ctggtagagc aggaaatcgt ggtactgctt atacatttat cacacccgac gaagagagat
1141 tctcttcgtc aatcattaaa gctttggaac aatctggttc aaaagtaccc gatgaactta
1201 gaaaattgaa tgatacctac gagaaaaaga gaaaagaagg taaggatgta ctattggcac
1261 caaccggttt cactggtaga ggtcataaat ttgatgctgc cgaagaggat aaaaagaata
1321 ttgaaagaaa acaacaaaga aaagcatatg gtatcgaaga ggaagaagaa gaagaggatg
1381 aagataaaga aaaagctgaa aaggagaaat tggccgctgc ttccgctgaa aaagaaaaac
1441 aattattatc tgaaaaagaa aaattggatc ctgctaccac taatactatc gtcatacctg
1501 gtgtagatgg tacaatcatt acaccttctt cattacttca aaccgatcct tcagttcctg
1561 tgggtcaaca ggctatcaat caaatatttg gtatttcaca agttacctcc tccgaagaag
1621 caattaaaaa acttcaattg gccgctcaat taggtatgaa aggtaatatt caaaaattaa
1681 ataatcaaat aactccatta aatcaaactc atttcattga agaattagaa attaatgatt
1741 cggaattc
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//

1: P09052[gi:1352826] This record was replaced or removed. See revision history for details.

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LOCUS       P09052                  661 aa            linear   INV 01-FEB-1996
DEFINITION  VASA PROTEIN.
ACCESSION   P09052
VERSION     P09052  GI:1352826
DBSOURCE    swissprot: locus VASA_DROME, accession P09052;
            class: standard.
            created: Nov 1, 1988.
            sequence updated: Feb 1, 1996.
            annotation updated: Feb 1, 1996.
            xrefs: gi: 433675, gi: 1054723, gi: 8804, gi: 84895, gi: 84894
            xrefs (non-sequence databases): FLYBASEFBgn0003970, PFAMPF00270,
            PFAMPF00271, PROSITEPS00039
KEYWORDS    Developmental protein; ATP-binding; Repeat; Helicase.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (residues 1 to 661)
  AUTHORS   Lasko,P.F. and Ashburner,M.
  TITLE     The product of the Drosophila gene vasa is very similar to
            eukaryotic initiation factor-4A
  JOURNAL   Nature 335 (6191), 611-617 (1988)
  MEDLINE   89014721
  REMARK    SEQUENCE FROM N.A.
REFERENCE   2  (residues 1 to 661)
  AUTHORS   LASKO,P.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (~DEC-1993)
  REMARK    REVISIONS.
REFERENCE   3  (residues 1 to 661)
  AUTHORS   Hay,B., Jan,L.Y. and Jan,Y.N.
  TITLE     A protein component of Drosophila polar granules is encoded by vasa
            and has extensive sequence similarity to ATP-dependent helicases
  JOURNAL   Cell 55 (4), 577-587 (1988)
  MEDLINE   89028669
  REMARK    SEQUENCE FROM N.A.
COMMENT     [WARNING] On Feb 1, 2001 this sequence was replaced by a newer
            version gi:12644110.
            On Jun 4, 1996 this sequence version replaced gi:137452.
            ---------------------------------------------------------------
            This SWISS-PROT entry is copyright. It is produced through a
            collaboration between the Swiss Institute of Bioinformatics and
            the EMBL outstation - the European Bioinformatics Institute.
            The original entry is available from http://www.expasy.ch/sprot
            and http://www.ebi.ac.uk/sprot
            ---------------------------------------------------------------.
            [FUNCTION] THE VASA PROTEIN IS REQUIRED ONLY IN THE FEMALE GERM
            LINE. IT IS IMPORTANT FOR OOCYTE FORMATION AND IN THE SPECIFICATION
            OF THE POSTERIOR STRUCTURES OF THE EMBRYO.
            [DEVELOPMENTAL STAGE] MATERNALLY EXPRESSED (DURING OOGENESIS).
            FUNCTION DURING EARLY EMBRYOGENESIS.
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          [SIMILARITY] TO OTHER 'DEAD' BOX FAMILY HELICASES.
FEATURES             Location/Qualifiers
     source          1..661
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
     gene            1..661
                     /gene="VAS"
     Protein         1..661
                     /gene="VAS"
                     /product="VASA PROTEIN"
     Region          35
                     /gene="VAS"
                     /region_name="Conflict"
                     /note="A -> R (IN REF. 3)."
     Region          93..127
                     /gene="VAS"
                     /region_name="Domain"
                     /note="5 X 7 AA TANDEM REPEATS OF [FS]-R-G-G- [EQ]-G-G."
     Region          93..99
                     /gene="VAS"
                     /region_name="Repetitive region"
                     /note="1."
     Region          100..106
                     /gene="VAS"
                     /region_name="Repetitive region"
                     /note="2."
     Region          107..113
                     /gene="VAS"
                     /region_name="Repetitive region"
                     /note="3."
     Region          114..120
                     /gene="VAS"
                     /region_name="Repetitive region"
                     /note="4."
     Region          121..127
                     /gene="VAS"
                     /region_name="Repetitive region"
                     /note="5."
     Region          265
                     /gene="VAS"
                     /region_name="Conflict"
                     /note="F -> Y (IN REF. 3)."
     Site            289..296
                     /gene="VAS"
                     /site_type="np-binding"
                     /note="ATP (BY SIMILARITY)."
     Site            399..402
                     /gene="VAS"
                     /site_type="unclassified"
                     /note="DEAD BOX."
     Region          582
                     /gene="VAS"
                     /region_name="Conflict"
                     /note="C -> R (IN REF. 3)."
     Region          594
                     /gene="VAS"
                     /region_name="Conflict"
                     /note="D -> H (IN REF. 3)."
     Region          644
                     /gene="VAS"
                     /region_name="Conflict"
                     /note="R -> RQ (IN REF. 3)."
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121 frggeggfrg rlyenedgde rrgrldreer ggerrgrldr eerggerger gdggfarrrr
181 neddinnnnn iaedverkre fyippepsnd aieifssgia sgihfskynn ipvkvtgsdv
241 pqpiqhftsa dlrdiiidnv nksgfkiptp iqkcsipvis sgrdlmacaq tgsgktaafl
301 lpilsklled phelelgrpq vvivsptrel aiqifneark fafesylkig ivyggtsfrh
361 qnecitrgch vviatpgrll dfvdrtfitf edtrfvvlde adrmldmgfs edmrrimthv
421 tmrpehqtlm fsatfpeeiq rmageflkny vsvaigivgg acsdvkqtiy evnkyakrsk
481 lieilseqad gtivfvetkr gadflasfls ekefpttsih gdrlqsqreq alrdfkngsm
541 kvliatsvas rgldiknikh vinydmpski ddyvhrigrt gcvgnngrat sffdpekdra
601 iaadlvkile gsgqtvpdfl rtcgaggdgg ysnqnfggvd vrgrgnyvgd atnveeeeqw
661 d
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24

1: Q64060. DEAD-box protein ...[gi:2500526] BLink, Domains, Links

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LOCUS       Q64060                    713 aa            linear   ROD 01-NOV-1997
DEFINITION  DEAD BOX PROTEIN 4 (VASA HOMOLOG) (RVLG).
ACCESSION   Q64060
VERSION     Q64060  GI:2500526
OBSOURCE    swissprot: locus DDX4_RAT, accession Q64060;
            class: standard.
            created: Nov 1, 1997.
            sequence updated: Nov 1, 1997.
            annotation updated: Nov 1, 1997.
            xrefs: gi: 806463, gi: 806464
            xrefs (non-sequence databases): PFAMPF00270, PFAMPF00271,
            PROSITEPS00039
KEYWORDS    ATP-binding; Helicase; RNA-binding.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE   1  (residues 1 to 713)
  AUTHORS   Komiya,T. and Tanigawa,Y.
  TITLE     Cloning of a gene of the DEAD box protein family which is
            specifically expressed in germ cells in rats
  JOURNAL   Biochem. Biophys. Res. Commun. 207 (1), 405-410 (1995)
  MEDLINE   95160706
  REMARK    SEQUENCE FROM N.A.
            STRAIN=WISTAR; TISSUE=TESTIS
COMMENT     ---------------------------------------------------------------------
            This SWISS-PROT entry is copyright. It is produced through a
            collaboration between the Swiss Institute of Bioinformatics and
            the EMBL outstation - the European Bioinformatics Institute.
            The original entry is available from http://www.expasy.ch/sprot
            and http://www.ebi.ac.uk/sprot
            ---------------------------------------------------------------------.
            [TISSUE SPECIFICITY] TESTIS.
            [SIMILARITY] TO OTHER 'DEAD' BOX FAMILY HELICASES. HIGHEST TO
            DROSOPHILA VASA.
FEATURES             Location/Qualifiers
     source          1..713
                     /organism="Rattus norvegicus"
                     /db_xref="taxon:10116"
     gene            1..713
                     /gene="DDX4"
     Protein         1..713
                     /gene="DDX4"
                     /product="DEAD BOX PROTEIN 4"
     Site            317..324
                     /gene="DDX4"
                     /site_type="np-binding"
                     /note="ATP (POTENTIAL)."
     Site            431..434
                     /gene="DDX4"
                     /site_type="unclassified"
                     /note="DEAD BOX."
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ORIGIN

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        1 mgdedweaei lkphvssyvp vfekdkyssg angdtfnrts asssemedgp sgrdhfmrsg
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      121 dtqtrsrgfs krggypdgnd seasgpfrrg grdseydqdq gsqrggglfg srkpaasdsg
      181 sgdtfqsrsg nargaykgln eevvtgsgkn swkseaegge ssdiqgpkvt yipppppede
      241 dsifahyqtg infdkydtil vevsghdapp ailtfeeanl cqtlnnniak agytkltpvq
      301 kysipivlag rdlmacaqtg sgktaafllp ilahmmrdgi tasrfkelqe peciivaptr
      361 elinqiylea rkfsfgtcvr avviyggtqf ghsirqivqg cnilcatpgr lmdiigkeki
      421 glkqvkylvl deadrmldmg fgpemkklis cpgmpskeqr qtllfsatfp eeiqrlagef
      481 lksnylfvav gqvggacrdv qqsilqvgpv fkkrklveil rnigderpmv fvetkkkadf
      541 iatflcqeki sttsihgdre qrereqalgd frcgkcpvlv atsvaargld ienvqhvinf
      601 nlpstideyv hrigrtgrcg ntgraisffd tesdnhlaqp lvkvlsdaqq dvpawleeia
      661 fssyappsfs nstrgavfas fdtrknfqgk ntlntagiss aqapnpvdde swd
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25

1: Q61496[gi:2500525] This record was replaced or removed. See revision history for details.

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LOCUS       Q61496                  637 aa            linear   ROD 01-NOV-1997
DEFINITION  DEAD BOX PROTEIN 4 (VASA HOMOLOG) (MVH).
ACCESSION   Q61496
VERSION     Q61496  GI:2500525
DBSOURCE    swissprot: locus DDX4_MOUSE, accession Q61496;
            class: standard.
            created: Nov 1, 1997.
            sequence updated: Nov 1, 1997.
            annotation updated: Nov 1, 1997.
            xrefs: gi: 286074, gi: 286075
            xrefs (non-sequence databases): MGI102670, PFAMPF00270,
            PFAMPF00271, PROSITEPS00039
KEYWORDS    ATP-binding; Helicase; RNA-binding.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (residues 1 to 637)
  AUTHORS   Fujiwara,Y., Komiya,T., Kawabata,H., Sato,M., Fujimoto,H.,
            Furusawa,M. and Noce,T.
  TITLE     Isolation of a DEAD-family protein gene that encodes a murine
            homolog of Drosophila vasa and its specific expression in germ cell
            lineage
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 91 (25), 12258-12262 (1994)
  MEDLINE   95083681
  REMARK    SEQUENCE FROM N.A.
            STRAIN=BALB/C; TISSUE=TESTIS
COMMENT     ---------------------------------------------------------------------
            This SWISS-PROT entry is copyright. It is produced through a
            collaboration between the Swiss Institute of Bioinformatics and
            the EMBL outstation - the European Bioinformatics Institute.
            The original entry is available from http://www.expasy.ch/sprot
            and http://www.ebi.ac.uk/sprot
            ---------------------------------------------------------------------.
            [SUBCELLULAR LOCATION] CYTOPLASMIC AND PERINUCLEAR.
            [TISSUE SPECIFICITY] TESTIS.
            [DEVELOPMENTAL STAGE] EXPRESSED IN SPERMATOGENIC CELLS FROM THE
            SPERMATOCYTE STAGE TO THE ROUND SPERMATID STAGE.
            [SIMILARITY] TO OTHER 'DEAD' BOX FAMILY HELICASES. HIGHEST TO
            DROSOPHILA VASA.
FEATURES             Location/Qualifiers
     source          1..637
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
     gene            1..637
                     /gene="DDX4"
                     /note="synonym: MVH"
     Protein         <1..637
                     /gene="DDX4"
                     /product="DEAD BOX PROTEIN 4"
     Site            246..253
                     /gene="DDX4"
```

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                     /site_type="np-binding"
                     /note="ATP (BY SIMILARITY)."
     Site            360..363
                     /gene="DDX4"
                     /site_type="unclassified"
                     /note="DEAD BOX."
ORIGIN
        1 fgrgkgfgnr gflnnkfeeg dssgfwkesn ndcednqtrs rgfskrggcq dgndseasgp
       61 frrggrgsfr gcrggfglgr pnsesdqdqg tqcgggflvl gkpaasdsgn gdtyqsrsgs
      121 grggykglne evvtgsgkns wksetegges sdsqgpkvty ipppppeded sifahyqtgi
      181 nfdkydtilv evsghdappa iltfeeanlc qtlnnnirka gytkltpvqk ytipivlagr
      241 dlmacaqtgs gktaafllpi lahmmrdgit asrfkelqep eciivaptre linqiylear
      301 kfsfgtcvis vviyggtqfg hsvrqivqgc nilcatpgrl mdiigkekig lkqvkylvld
      361 eadsmldmgf apeikklisc pgmpskeqhq tllfsatfpe eiqrlagdfl ksnylfvavg
      421 qvggacrdvq qtilqvgqyq keksllrfye nigdertmvf vetkkkadfi atflcqekis
      481 stsihgdreq rereqalgdf rcgkcpvlva tsvaargldi envqhvinfd lpstideyvh
      541 rigrtgrcgn tgraisffdt dsdnhlaqpl vkvlsdaqqd vpawleeiaf styvppsfss
      601 strggavfas vdtrknyqgk ahveysgdff ftssqss
//
```

(26)

1: Q62167. DEAD-box protein ...[gi:2500528]


```
LOCUS       Q62167                    662 aa            linear   ROD 15-JUL-1999
DEFINITION  DEAD BOX PROTEIN 3 (DEAD-BOX RNA HELICASE DEAD3) (MDEAD3)
            (EMBRYONIC RNA HELICASE) (D1PAS1 RELATED SEQUENCE 2).
ACCESSION   Q62167
VERSION     Q62167  GI:2500528
DBSOURCE    swissprot: locus DDX3_MOUSE, accession Q62167;
            class: standard.
            extra accessions:O09060,O09143,created: Nov 1, 1997.
            sequence updated: Nov 1, 1997.
            annotation updated: Jul 15, 1999.
            xrefs: gi: 1835121, gi: 1835122, gi: 407995, gi: 407996
            xrefs (non-sequence databases): MGI103064, PFAMPF00270,
            PFAMPF00271, PROSITEPS00039
KEYWORDS    Helicase; ATP-binding; RNA-binding; DNA-binding.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (residues 1 to 662)
  AUTHORS   Sowden,J., Putt,W., Morrison,K., Beddington,R. and Edwards,Y.
  TITLE     The embryonic RNA helicase gene (ERH): a new member of the DEAD box
            family of RNA helicases
  JOURNAL   Biochem. J. 308 (Pt 3), 839-846 (1995)
  MEDLINE   97104282
  REMARK    SEQUENCE FROM N.A.
            STRAIN=C57BL/6, AND DBA
REFERENCE   2  (residues 1 to 662)
  AUTHORS   Gee,S.L. and Conboy,J.G.
  TITLE     Mouse erythroid cells express multiple putative RNA helicase genes
            exhibiting high sequence conservation from yeast to mammals
  JOURNAL   Gene 140 (2), 171-177 (1994)
  MEDLINE   94192995
  REMARK    SEQUENCE FROM N.A.
            TISSUE=ERYTHROLEUKEMIA
COMMENT     ---------------------------------------------------------------------
            This SWISS-PROT entry is copyright. It is produced through a
            collaboration between the Swiss Institute of Bioinformatics and
            the EMBL outstation - the European Bioinformatics Institute.
            The original entry is available from http://www.expasy.ch/sprot
            and http://www.ebi.ac.uk/sprot
            ---------------------------------------------------------------------.
            [FUNCTION] PUTATIVE ATP-DEPENDENT RNA HELICASE. IT MAY PLAY A ROLE
            IN TRANSLATIONAL ACTIVATION OF MRNA IN THE OOCYTE AND EARLY EMBRYO.
            [TISSUE SPECIFICITY] DEVELOPMENTALLY REGULATED.
            [DEVELOPMENTAL STAGE] EXPRESSED IN OOCYTES. UBIQUITOUSLY FOUND IN 9
            DAYS POST-CONCEPTION EMBRYO, AT LATER STAGES IT IS RESTRICTED TO
            BRAIN AND KIDNEY.
            [SIMILARITY] TO OTHER 'DEAD' BOX FAMILY HELICASES. BELONGS TO THE
            PL10 SUBFAMILY.
FEATURES              Location/Qualifiers
     source           1..662
                      /organism="Mus musculus"
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                     /db_xref="taxon:10090"
     gene            1..662
                     /gene="DDX3"
                     /note="synonyms: DEAD3, ERH, D1PAS1-RS2"
     Protein         1..662
                     /gene="DDX3"
                     /product="DEAD BOX PROTEIN 3"
     Site            224..231
                     /gene="DDX3"
                     /site_type="np-binding"
                     /note="ATP (POTENTIAL)."
     Site            347..350
                     /gene="DDX3"
                     /site_type="unclassified"
                     /note="DEAD BOX."
     Region          582..662
                     /gene="DDX3"
                     /region_name="Domain"
                     /note="GLY/SER-RICH."
     Region          609..616
                     /gene="DDX3"
                     /region_name="Domain"
                     /note="POLY-SER."
     Region          624..630
                     /gene="DDX3"
                     /region_name="Domain"
                     /note="POLY-GLY."
     Region          633..641
                     /gene="DDX3"
                     /region_name="Domain"
                     /note="POLY-GLY."
ORIGIN
        1 mshvavenal gldqqfagld lnssdnqsgg staskgryip phlrnreatk gfydkdssgw
       61 ssskdkdays sfgsrgdsrg kssffgdrgs gsrgrfddrg rgdydgiggr gdrsgfgkfe
      121 rggnsrwcdk sdeddwskpl ppserleqel fsggntginf ekyddipvea tgnncpphie
      181 sfsdvemgei imgnieltry trptpvqkha ipiikekrdl macaqtgsgk taafllpils
      241 qiyadgpgea lramkengry grrkqypisl vlaptrelav qiyeearkfs yrsrvrpcvv
      301 yggaeigqqi rdlergchll vatpgrlvdm mergkigldf ckylvldead rmldmgfepq
      361 irriveqdtm ppkgvrhtmm fsatfpkeiq mlardfldey iflavgrvgs tsenitqkvv
      421 wveeidkrsf lldllnatgk dsltlvfvet kkgadsledf lyhegyacts ihgdrsqrdr
      481 eealhqfrsg kspilvatav aargldisnv khvinfdlps dieeyvhrig rtgrvgnlgl
      541 atsffnerni nitkdlldll veakqevpsw lenmafehhy kgssrgrsks srfsggfgar
      601 dyrqssgass ssfsssrass srsgggghgg srgfggggyg gfynsdgygg nynsqgvdww
      661 gn
//
```

(27)

1: O00571. DEAD-box protein ...[gi:3023628]


```
LOCUS       O00571                  662 aa            linear   PRI 15-JUL-1999
DEFINITION  DEAD BOX PROTEIN 3 (HELICASE-LIKE PROTEIN 2) (HLP2) (DEAD BOX, X
            ISOFORM).
ACCESSION   O00571
VERSION     O00571  GI:3023628
DBSOURCE    swissprot: locus DDX3_HUMAN, accession O00571;
            class: standard.
            extra accessions:O15536,created: Jul 15, 1998.
            sequence updated: Jul 15, 1998.
            annotation updated: Jul 15, 1999.
            xrefs: gi: 2148923, gi: 2148924, gi: 3523149, gi: 3523150, gi:
            2580551, gi: 2580552, gi: 2580549, gi: 2580550
            xrefs (non-sequence databases): MIM 300160, PFAMPF00270,
            PFAMPF00271, PROSITEPS00039
KEYWORDS    Helicase; ATP-binding; RNA-binding; DNA-binding.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (residues 1 to 662)
  AUTHORS   CHUNG,J., LEE,S.-G. and SONG,K.
  TITLE     Identification of a human homolog of a putative RNA helicase gene
            (mDEAD3) expressed in mouse erythroid cells
  JOURNAL   Korean J. Biochem. 27, 193-197 (1995)
  REMARK    SEQUENCE FROM N.A.
            TISSUE=LIVER, AND HIPPOCAMPUS
REFERENCE   2  (residues 1 to 662)
  AUTHORS   OWSIANKA,A.M. and PATEL,A.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (~APR-1998)
  REMARK    SEQUENCE FROM N.A.
REFERENCE   3  (residues 1 to 662)
  AUTHORS   Lahn,B.T. and Page,D.C.
  TITLE     Functional coherence of the human Y chromosome
  JOURNAL   Science 278 (5338), 675-680 (1997)
  MEDLINE   98022381
  REMARK    SEQUENCE FROM N.A.
COMMENT     ---------------------------------------------------------------------
            This SWISS-PROT entry is copyright. It is produced through a
            collaboration between the Swiss Institute of Bioinformatics and
            the EMBL outstation - the European Bioinformatics Institute.
            The original entry is available from http://www.expasy.ch/sprot
            and http://www.ebi.ac.uk/sprot
            ---------------------------------------------------------------------.
            [FUNCTION] PUTATIVE ATP-DEPENDENT RNA HELICASE. INTERACTS
            SPECIFICALLY WITH HEPATITIS C VIRUS CORE PROTEIN RESULTING A CHANGE
            IN INTRACELLULAR LOCATION.
            [SIMILARITY] TO OTHER 'DEAD' BOX FAMILY HELICASES. BELONGS TO THE
            PL10 SUBFAMILY.
FEATURES                Location/Qualifiers
     source             1..662
                        /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
     gene            1..662
                     /gene="DDX3"
                     /note="synonym: DBX"
     Protein         1..662
                     /gene="DDX3"
                     /product="DEAD BOX PROTEIN 3"
     Region          50
                     /gene="DDX3"
                     /region_name="Conflict"
                     /note="K -> R (IN REF. 3)."
     Site            224..231
                     /gene="DDX3"
                     /site_type="np-binding"
                     /note="ATP (POTENTIAL)."
     Site            347..350
                     /gene="DDX3"
                     /site_type="unclassified"
                     /note="DEAD BOX."
     Region          582..662
                     /gene="DDX3"
                     /region_name="Domain"
                     /note="GLY/SER-RICH."
ORIGIN
        1 mshvavenal gldqqfagld lnssdnqsgg staskgryip phlrnreatk gfydkdssgw
       61 ssskdkdays sfgsrsdsrg kssffsdrgs gsrgrfddrg rsdydgigsr gdrsgfgkfe
      121 rggnsrwcdk sdeddwskpl ppserleqel fsggntginf ekyddipvea tgnncpphie
      181 sfsdvemgei imgnieltry trptpvqkha ipiikekrdl macaqtgsgk taafllpils
      241 qiysdgpgea lramkengry grrkqypisl vlaptrelav qiyeearkfs yrsrvrpcvv
      301 yggadigqqi rdlergchll vatpgrlvdm mergkigldf ckylvldead rmldmgfepq
      361 irriveqdtm ppkgvrhtmm fsatfpkeiq mlardfldey iflavgrvgs tsenitqkvv
      421 wveesdkrsf lldllnatgk dsltlvfvet kkgadsledf lyhegyacts ihgdrsqrdr
      481 eealhqfrsg kspilvatav aargldisnv khvinfdlps dieeyvhrig rtgrvgnlgl
      541 atsffnerni nitkdlldll veakqevpsw lenmayehhy kgssrgrsks srfsggfgar
      601 dyrqssgass ssfsssrass srsgggghgs srgfggggyg gfynsdgygg nynsqgvdww
      661 gn
//
```

28

1: P24346. Putative ATP-depe...[gi:113825] BLink, Domains, Links

```
LOCUS       P24346                  697 aa            linear   VRT 01-FEB-1996
DEFINITION  PUTATIVE ATP-DEPENDENT RNA HELICASE AN3.
ACCESSION   P24346
VERSION     P24346  GI:113825
DBSOURCE    swissprot: locus AN3_XENLA, accession P24346;
            class: standard.
            created: Mar 1, 1992.
            sequence updated: Mar 1, 1992.
            annotation updated: Feb 1, 1996.
            xrefs: gi: 65059, gi: 65060, gi: 103989, gi: 345587
            xrefs (non-sequence databases): PFAMPF00270, PFAMPF00271,
            PROSITEPS00039
KEYWORDS    Helicase; ATP-binding; RNA-binding.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
            Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
            Xenopus.
REFERENCE   1  (residues 1 to 697)
  AUTHORS   Gururajan,R., Perry-O'Keefe,H., Melton,D.A. and Weeks,D.L.
  TITLE     The Xenopus localized messenger RNA An3 may encode an ATP-dependent
            RNA helicase
  JOURNAL   Nature 349 (6311), 717-719 (1991)
  MEDLINE   91141586
  REMARK    SEQUENCE FROM N.A.
COMMENT     ---------------------------------------------------------------------
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            collaboration between the Swiss Institute of Bioinformatics and
            the EMBL outstation - the European Bioinformatics Institute.
            The original entry is available from http://www.expasy.ch/sprot
            and http://www.ebi.ac.uk/sprot
            ---------------------------------------------------------------------.
            [FUNCTION] PUTATIVE ATP-DEPENDENT RNA HELICASE.
            [SIMILARITY] TO OTHER 'DEAD' BOX FAMILY HELICASES. BELONGS TO THE
            PL10 SUBFAMILY.
FEATURES             Location/Qualifiers
     source          1..697
                     /organism="Xenopus laevis"
                     /db_xref="taxon:8355"
     gene            1..697
                     /gene="AN3"
     Protein         1..697
                     /gene="AN3"
                     /product="PUTATIVE ATP-DEPENDENT RNA HELICASE AN3"
     Site            265..272
                     /gene="AN3"
                     /site_type="np-binding"
                     /note="ATP (BY SIMILARITY)."
     Site            388..391
                     /gene="AN3"
                     /site_type="unclassified"
                     /note="DEAD BOX."
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     Region           623..697
                      /gene="AN3"
                      /region_name="Domain"
                      /note="GLY/SER-RICH."
ORIGIN
        1 mshvavenvl nldqqfagld lnsadaesgv agtkgryipp hlrnkeasrn dsnwdsgrgg
       61 ngyingmqdd rdgrmngydr ggygsrgtgr sdrgfydren sgwnsgrdkd ayssfgsrgd
      121 rgkgslfner gsgsrrtddr rqdgfdgmgn rsdksgfgrf drgnsrwsdd rndeddwskp
      181 lapndrveqe lfsgsntgin fekyddipve atgsncpphi esfhdvtmge iimgniqltr
      241 ytrptpvqkh aipiiiekrd lmacaqtgsg ktaafllpil sqiyadgpgd amkhlqengr
      301 ygrrkqfpls lvlaptrela vqiyeearkf ayrsrvrpcv vyggadigqq irdlergchl
      361 lvatpgrlvd mmergkigld fckylvldea drmldmgfep qirriveqdt mppkgvrqtm
      421 mfsatfpkei qilardflde yiflavgrvg stsenitqkv vwveemdkrs flldllnatg
      481 kdsltlvfve tkkgadaled flyhegyact sihgdrsqrd reealhqfrs gkspilvata
      541 vaargldisn vkhvinfdlp sdieeyvhri grtgrvgnlg latsffnekn initkdlldl
      601 lveakqevps wlenmayeqh hksssrgrsk srfsggfgak dyrqssgags sfgssrggrs
      661 sghggsrgfg ggyggfynsd gyggnyggss qvdwwgn
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```

29

1: P16381. Putative ATP-depe...[gi:130256]


```
LOCUS       P16381                    660 aa            linear   ROD 15-JUL-1999
DEFINITION  PUTATIVE ATP-DEPENDENT RNA HELICASE PL10.
ACCESSION   P16381
VERSION     P16381  GI:130256
DBSOURCE    swissprot: locus PL10_MOUSE, accession P16381;
            class: standard.
            created: Aug 1, 1990.
            sequence updated: Aug 1, 1990.
            annotation updated: Jul 15, 1999.
            xrefs: gi: 200388, gi: 200389, gi: 110038
            xrefs (non-sequence databases): PFAMPF00270, PFAMPF00271,
            PROSITEPS00039
KEYWORDS    Helicase; ATP-binding; RNA-binding; DNA-binding; Spermatogenesis.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (residues 1 to 660)
  AUTHORS   Leroy,P., Alzari,P., Sassoon,D., Wolgemuth,D. and Fellous,M.
  TITLE     The protein encoded by a murine male germ cell-specific transcript
            is a putative ATP-dependent RNA helicase
  JOURNAL   Cell 57 (4), 549-559 (1989)
  MEDLINE   89249320
  REMARK    SEQUENCE FROM N.A.
            TISSUE=TESTIS
COMMENT     ---------------------------------------------------------------
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            collaboration between the Swiss Institute of Bioinformatics and
            the EMBL outstation - the European Bioinformatics Institute.
            The original entry is available from http://www.expasy.ch/sprot
            and http://www.ebi.ac.uk/sprot
            ---------------------------------------------------------------.
            [FUNCTION] PUTATIVE ATP-DEPENDENT RNA HELICASE. POSSIBLE ROLE IN A
            KEY STEP OF THE SPERMATOGENIC PROCESS.
            [TISSUE SPECIFICITY] TESTIS.
            [DEVELOPMENTAL STAGE] HIGH LEVELS OF PL10 DURING THE MEIOTIC AND
            HAPLOID STAGES OF SPERMATOGENESIS.
            [SIMILARITY] TO OTHER 'DEAD' BOX FAMILY HELICASES. BELONGS TO THE
            PL10 SUBFAMILY.
FEATURES             Location/Qualifiers
     source          1..660
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
     gene            1..660
                     /gene="PL10"
                     /note="synonym: D1PAS1"
     Protein         1..660
                     /gene="PL10"
                     /product="PUTATIVE ATP-DEPENDENT RNA HELICASE PL10"
     Site            223..230
                     /gene="PL10"
                     /site_type="np-binding"
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                     /note="ATP (POTENTIAL)."
     Site            346..349
                     /gene="PL10"
                     /site_type="unclassified"
                     /note="DEAD BOX."
     Site            495..514
                     /gene="PL10"
                     /site_type="DNA binding"
                     /note="POTENTIAL."
     Region          581..660
                     /gene="PL10"
                     /region_name="Domain"
                     /note="GLY/SER-RICH."
ORIGIN
        1 mshvaeedel gldqqlagld ltsrdsqsgg staskgryip phlrnreaak afydkdgsrw
       61 skdkdayssf gsrsdtraks sffsdrggsg srgrfdergr sdyesvgsrg grsgfgkfer
      121 ggnsrwcdka deddwskplp pserleqelf sggntginfe kyddipveat gnncpphies
      181 fsdvemgeii mgnieltryt rptpvqkhai piikekrdlm acaqtgsgkt aafllpilsq
      241 iytdgpgeal ramkengkyg rrkqypislv laptrelavq iyeearkfsy rsrvrpcvvy
      301 ggadigqqir dlergchllv atpgrlvdmm ergkigldfc kylvldeadr mldmgfepqi
      361 rriveqdtmp pkgvrhtmmf satfpkeiqm lardfldeyi flavgrvgst senitqkvvw
      421 veeadkrsfl ldllnatgkd slilvfvetk kgadsledfl yhegyactsi hgdrsqrdre
      481 ealhqfrsgk spilvatava argldisnvk hvinfdlpsd ieeyvhrigr tgrvgnlgla
      541 tsffnernin itkdlldllv eakqevpswl enmafehhyk ggsrgrsksr fsggfgardy
      601 rqssgassss fssgrasnsr sgggshgssr gfgggsyggf ynsdgyggny ssqgvdwwgn
//
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1: O15523. DEAD-box protein ...[gi:6014945]

BLink, Domains, Links

```
LOCUS       O15523                   660 aa            linear   PRI 15-JUL-1999
DEFINITION  DEAD BOX PROTEIN 3, Y-CHROMOSOMAL.
ACCESSION   O15523
VERSION     O15523  GI:6014945
DBSOURCE    swissprot: locus DDXY_HUMAN, accession O15523;
            class: standard.
            created: Jul 15, 1999.
            sequence updated: Jul 15, 1999.
            annotation updated: Jul 15, 1999.
            xrefs: gi: 2580555, gi: 2580556, gi: 2580553, gi: 2580554
            xrefs (non-sequence databases): MIM 400010, PFAMPF00270,
            PFAMPF00271, PROSITEPS00039
KEYWORDS    Helicase; ATP-binding; RNA-binding; DNA-binding.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (residues 1 to 660)
  AUTHORS   Lahn,B.T. and Page,D.C.
  TITLE     Functional coherence of the human Y chromosome
  JOURNAL   Science 278 (5338), 675-680 (1997)
  MEDLINE   98022381
  REMARK    SEQUENCE FROM N.A.
COMMENT     ---------------------------------------------------------------------
            This SWISS-PROT entry is copyright. It is produced through a
            collaboration between the Swiss Institute of Bioinformatics and
            the EMBL outstation - the European Bioinformatics Institute.
            The original entry is available from http://www.expasy.ch/sprot
            and http://www.ebi.ac.uk/sprot
            ---------------------------------------------------------------------.
            [SIMILARITY] TO OTHER 'DEAD' BOX FAMILY HELICASES. BELONGS TO THE
            PL10 SUBFAMILY.
FEATURES             Location/Qualifiers
     source          1..660
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     gene            1..660
                     /gene="DBY"
     Protein         1..660
                     /gene="DBY"
                     /product="DEAD BOX PROTEIN 3, Y-CHROMOSOMAL"
     Site            222..229
                     /gene="DBY"
                     /site_type="np-binding"
                     /note="ATP (POTENTIAL)."
     Site            345..348
                     /gene="DBY"
                     /site_type="unclassified"
                     /note="DEAD BOX."
ORIGIN
        1 mshvvvkndp eldqqlanld lnsekqsgga staskgryip phlrnkeask gfhdkdssgw
       61 scskdkdays sfgsrdsrgk pgyfsergsg srgrfddrgr sdydgignre rpgfgrfers
```

```
121 ghsrwcdksv eddwskplpp serleqelfs ggntginfek yddipveatg sncpphienf
181 sdidmgeiim gnieltrytr ptpvqkhaip iikgkrdlva caqtgsgkta afllpilsqi
241 ytdgpgealk avkengrygr rkqypislvl aptrelavqi yeearkfsyr srvrpcvvyg
301 gadigqqird lergchllva tpgrlvdmme rgkigldfck ylvldeadrm ldmgfepqir
361 riveqdtmpp kgvrhtmmfs atfpkeiqml ardfldeyif lavgrvgsts enitqkvvwv
421 edldkrsfll dilgatgsds ltlvfvetkk gadsledfly hegyactsih gdrsqrdree
481 alhqfrsgks pilvatavaa rgldisnvrh vinfdlpsdi eeyvhrigrt grvgnlglat
541 sffneknmni tkdlldllve akqevpswle nmayehhykg gsrgrsksnr fsggfgardy
601 rqssgssssg fgasrgsssr sggggygdsr gfgggggyggf ynsdgyggny nsqgvdwwgn
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1: AL042306. DKFZp434M0720_r1 ...[gi:5421648] Links

IDENTIFIERS

dbEST Id: **2890414**
EST name: DKFZp434M0720_r1
GenBank Acc: AL042306
GenBank gi: 5421648
Database: RZPD Cross Reference: DKFZp434M0720

CLONE INFO
Clone Id: DKFZp434M0720 (5')
DNA type: cDNA

PRIMERS
PolyA Tail: Unknown

SEQUENCE

GAGAACTTGAAGCCACCATGGGAGATGAAGATTGGGAAGCAGAAATCAACCCTCATATGT
CTTCCTATGTTCCCATATTTGAGAAGGATAGGTATTCTGGAGAAAATGGAGACAATTTTA
ACAGGACTCCAGCTTCATCATCAGAAATGGATGATGGACCTTCTCGAAGAGATCATTTCA
TGAAAAGTGGATTTGCCTCTGGGCGGAATTTTGGAAACAGAGATGCTGGTGAGTGTAATA
AGCGAGATAATACATCCACAATGGGTGGTTTTGGAGTTGGAAAGAGTTTTGGAAACAGAG
GTTTTTCAAACAGCAGGTTTGAAGATGGTGATAGCTCTTGTTTCTGGAGAGAGTCTAGTA
ATGACTGCGAAGATAATCCAACACGGAACAGAGGGGTTTTCAAGAAAGGCGGCTATCGAG
ATGGAAATAATTCAGAAGCTTCAGGGCCATACAGAGAGGTGGAGAGGTAGTTTTCCGAGG
TG

Entry Created: Jul 8 1999
Last Updated: Sep 4 2003

COMMENTS

This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by MediGenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project. No s1 sequence available.
This clone (DKFZp434M0720) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de

LIBRARY
Lib Name: 434 (synonym: htes3)
Organism: Homo sapiens
Tissue type: testis
Develop. stage: adult
Lab host: DH10B
Vector: pSport1
R. Site 1: NotI
R. Site 2: SalI

SUBMITTER

lame: MIPS
:nstitution: MIPS
\ddress: Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

:ITATIONS

:itle: EST (Ottenwaelder, et al.)
\uthors: Ottenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J., Wiemann,S.
(ear: 1999
3tatus: Unpublished

4AP DATA

Sequence Revision History

Revision history for AL042306

GI	Version	Update Date	Status
5421648	1	Jul 8 1999 7:06 PM	Live

Accession AL042306 was first seen at NCBI on Jul 8 1999 7:06 PM

Entrez

Search for Genes
LocusLink provides curated information for human, fruit fly, mouse, rat, and zebrafish

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BLAST

Reference sequence project

LocusLink

Clusters of orthologous groups

Protein reviews on the web

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NCBI | NLM|NIH

1: AA399611. zt93a07.s1 Soares...[gi:2052633] Links

IDENTIFIERS

dbEST Id:	**1040402**
EST name:	zt93a07.s1
GenBank Acc:	AA399611
GenBank gi:	2052633
GDB Id:	5926405

CLONE INFO

Clone Id:	IMAGE:729876 (3')
Source:	IMAGE Consortium, LLNL
DNA type:	cDNA

PRIMERS

Sequencing:	-41m13 fwd. ET from Amersham
PolyA Tail:	Unknown

SEQUENCE

TTTGACATTTAGAATGCTTTAATATTCCCAGTTAACACCATTTGTATCAGTAACTGCAAT
GTTGTAAGTTTTAGCATCTCACATAACTAGTCAGTAAGGATTTTTTTTTTAAGTGTAGGA
GTGAGAATACAAGGACAGGAGCTATGAGAATGTTAAGTTTTATACTTCTGTTAAAAACTC
AAAAATCAAAACTATTTTCTTCTCTGCATCAAAACCACAGACTTGAAGGATGTTTTGGCT
TTAATCCCATGACTCATCATCTACTGGATTGGGAGCTTGTGAAGAAGAAAACCCAGCTGT
GTTCAAAGTGCTCTTGCCCTTTCTGGTATCAACTGATGCAAACACGTTTCCTCTTGTACT
ACCACTGAAGCCAGGAATGTATGTACTAAAGGCAATTTCTTCCAACCATGCAGGAACATC
CTGTTGAGCATCTGTCAATACTTTTACTAGAGGCTGTGCTAAATGGTTATCCGATTCAAG
ATCAAAAAAGGAAATTGCTCTGCCAGTATTCCCACAACGACCAGTACGCCCAATTCGATG
AACATATTCATCAAT

Quality: High quality sequence stops at base: 474

Entry Created:	Apr 28 1997
Last Updated:	May 16 1997

COMMENTS

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand

PUTATIVE ID: Assigned by submitter
TR:G806464 G806464 VASA-LIKE GENE PROTEIN. ;

LIBRARY

Lib Name:	Soares_testis_NHT
Organism:	Homo sapiens
Sex:	male
Lab host:	DH10B
Vector:	pT7T3D-Pac (Pharmacia) with a modified polylinker
R. Site 1:	Not I
R. Site 2:	Eco RI
Description:	1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo

(dT) primer [5'
TGTTACCAATCTGAAGTGGGAGCGGCCGCCCAATTTTTTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library went
through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo.

SUBMITTER

Name: Wilson RK
Institution: Washington University School of Medicine
Address: 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
E-mail: est@watson.wustl.edu

CITATIONS

Title: WashU-Merck EST Project 1997
Authors: Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost
,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising
,B., White,Y., Wylie,T., Waterston,R., Wilson,R.
Year: 1997
Status: Unpublished

MAP DATA

1: AA398976. zt93a07.r1 Soares...[gi:2052713] Links

IDENTIFIERS

dbEST Id:	**1040482**
EST name:	zt93a07.r1
GenBank Acc:	AA398976
GenBank gi:	2052713
GDB Id:	5926405

CLONE INFO

Clone Id:	IMAGE:729876 (5')
Source:	IMAGE Consortium, LLNL
DNA type:	cDNA

PRIMERS

Sequencing:	-28m13 rev2 ET from Amersham
PolyA Tail:	Unknown

SEQUENCE

ATTGATGAATATGTTCATCGAATTGGGCGTACTGGTCGTTGTGGGAATACTGGCAGACAA
TTTCCTTTTTTGATCTTGAATCGGATAACCATTTAGCACAGCCTCTAGTAAAAGTATTGA
CAGATGCTCAACAGGATGTTCCTGCATGGTTGGAAGAAATTGCCTTTAGTACATACATTC
CTGGCTTCAGTGGTAGTACAAGAGGAAACGTGTTTGCATCAGTTGATACCAGAAAGGGCA
AGAGCACTTTGAACACAGCTGGGTTTTCTTCTTCACAAGCTCCCAATCCAGTAGATGATG
AGTCATGGGATTAAAGCCAAAACATCCTTCAAGTCTGTGGTTTTGATGCAGAGAAGAAAA
TAGTTTTGATTTTTGAGTTTTTAACAGAAGTATAAAACTTAACATTCTCATAGCTCCTGT
CCTTGTATTCTCACTCCTACACTTAAAAAAAAAATCCTTACTGACTAGTTATGTGAGATG
CTAAAACTTAC

Entry Created:	Apr 28 1997
Last Updated:	May 16 1997

COMMENTS

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Putative full length read
The vector to vector length is 554

PUTATIVE ID	Assigned by submitter TR:G286075 G286075 DROSOPHILA VASA HOMOLOGUE ;

LIBRARY

Lib Name:	Soares_testis_NHT
Organism:	Homo sapiens
Sex:	male
Lab host:	DH10B
Vector:	pT7T3D-Pac (Pharmacia) with a modified polylinker
R. Site 1:	Not I
R. Site 2:	Eco RI
Description:	1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo (dT) primer [5'

TGTTACCAATCTGAAGTGGGAGCGGCCGCCCAATTTTTTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library went
through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo.

SUBMITTER

Name: Wilson RK
Institution: Washington University School of Medicine
Address: 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
E-mail: est@watson.wustl.edu

CITATIONS

Title: WashU-Merck EST Project 1997
Authors: Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost
,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising
,B., White,Y., Wylie,T., Waterston,R., Wilson,R.
Year: 1997
Status: Unpublished

MAP DATA

34

1: AA383535. EST96928 Testis I...[gi:2035852] Links

IDENTIFIERS

dbEST Id:	**1024641**
EST name:	EST96928
GenBank Acc:	AA383535
GenBank gi:	2035852

CLONE INFO

Clone Id:	(5' end)
Source:	ATCC
Id in host:	187704
DNA type:	cDNA

PRIMERS

Sequencing:	M13 Reverse
PolyA Tail:	Unknown

SEQUENCE

TTATATATGGGGGAACCCAGCTGGGACATTCAATTCGACAAATAGTACAAGGCTGTAATA
TATTATGTGCTACTCCTGGAAGACTGATGGATATCATAGGCAAAGAAAAGATTGGTCTCA
AACAGATCAAATACTTAGTTTTGGATGAAGCTGATCGCATGTTGGATATGGGTTTTGGTC
CAGAAATGAAGAAGTTAATTNNTTGCCCAGGAATGCCATCAAAGGAACAGCGCCAAACCC
TTATGTTCAGTGCAACTTTTCCAGAGGAAATTCAAAGGTTGGCTGCAGAGTTTTTAAAGT
CAAATTATCTGTTTGTTGCTGTTGGACAAGTGGGT

Entry Created:	Apr 21 1997
Last Updated:	Apr 21 1997

COMMENTS

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)

PUTATIVE ID	Assigned by submitter similar to vasa homolog

LIBRARY

Lib Name:	Testis I
Organism:	Homo sapiens
Sex:	male
Organ:	testis
Develop. stage:	adult
Vector:	pBluescript SK-
R. Site 1:	EcoRI
R. Site 2:	XhoI

SUBMITTER

Name:	Kerlavage, AR
Lab:	Bioinformatics
Institution:	The Institute for Genomic Research
Address:	9712 Medical Center Drive, Rockville, MD 20850 USA
Tel:	3018699056

Fax: 3018699423
E-mail: arkerlav@tigr.org

CITATIONS

Medline UID: 96026280
Title: Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Authors: Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M., Venter,J.C.
Citation: Nature 377 (6547 Suppl): 3-174 1995

MAP DATA

ORIGIN

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        1 cttgcttcca accctggctc agggcgtcct aaccaggccc ggtagcctct ggggcagact
       61 taggccagag gctgctcaca tgggcctgcc tggggcttga ggtcggcctc tggggccttc
      121 ccgctcagac tggagtcttc atgctgagta gagcggtgtg tgaacacttg aggcctgcag
      181 gggagggagg cccagggaac cttctgctca gcgcctaggc ggccatttct cagaagaaac
      241 ggtgtttgtg gaacctgaag ctatcatggg agatgaagat tgggaggcag aaatcctcaa
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      361 tggagacact tttaacagga cttcagcttc atcatcagaa atggaagatg gaccttctgg
      421 aagagatcat ttcatgagaa gtggattttc ctctggaaga aatttaggaa acagagatat
      481 tggcgagtct agtaaaagag agactacatc tacaaccggt ggctttggaa gaggaaaggg
      541 ttttggaaac agaggttttt taaataacaa gtttgaagaa ggtgacagct ctggtttctg
      601 gaaagagtct actaatgact gtgaagatac tcagactcgg agcagagggt tttccaagcg
      661 aggcggctat ccagatggga atgattcgga agcttcaggc ccattcagaa gaggtgggag
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     1441 ctcaattcga cagatagtgc aagggtgtaa tatattatgt gctactccag ggaggctgat
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     1561 agctgatcga atgttggata tgggttttgg acccgaaatg aagaagttaa tttcttgtcc
     1621 aggaatgcca tcaaaggaac agcgccaaac tctcttattc agtgcaactt ttccagaaga
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     1741 agtgggagga gcttgcagag atgtgcagca gtccattctt caagttggcc cagtattcaa
     1801 aaagagaaaa cttgttgaga ttctacgaaa cataggtgat gaaagaccta tggtctttgt
     1861 tgaaaccaag aaaaaagcag atttcattgc gactttcctt tgtcaagaaa aaatatcaac
     1921 tacaagtatt catggcgatc gggaacagag ggagcgagaa caagctcttg gagattttcg
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     2101 aattggacgt actggacgtt gtggaaatac tggcagggcg atttcttttt ttgataccga
     2161 atctgataat catttagcac aacctctagt taaagtactg tcagatgctc aacaggatgt
     2221 tcctgcgtgg ttagaagaga ttgcctttag ttcatatgcg cctcccagct tcagtaatag
     2281 cacaagaggg gctgtgtttg catcttttga cactaggaag aatttccagg gcaagaacac
     2341 actgaacaca gctgggattt cttctgcaca agctcccaat ccagttgatg acgagtcatg
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     2521 tctgttctta ctcccaaccc ttaaaaaata accagcttca ttgattagtt atgcgaaatg
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     2881 tttttagatc atcagacatg taatgaaaat ggttcagttt gcaatgtgag ctctgtactt
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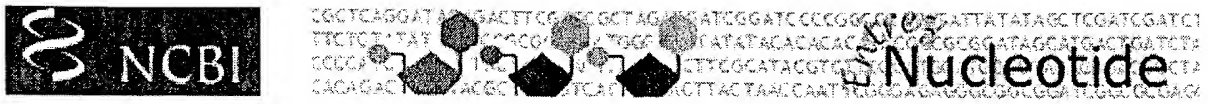

1: D14859. Mus musculus mRNA...[gi:286074]


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LOCUS       MUSDVH                  1930 bp    mRNA    linear   ROD 04-FEB-1999
DEFINITION  Mouse mRNA for drosophila vasa homologue, partial cds.
ACCESSION   D14859
VERSION     D14859.1  GI:286074
KEYWORDS    RNA helicase; drosophila vasa homologue.
SOURCE      Mus musculus
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1930)
  AUTHORS   Noce,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-APR-1993) Toshiaki Noce, Mitsubishi Kasei Institute
            of Life Sciences, Developmental Biology; 11 Minamiooya, Machida,
            Tokyo 194, Japan (Tel:0427-24-6246, Fax:0427-29-1252)
REFERENCE   2  (bases 1 to 1930)
  AUTHORS   Noce,T.
  JOURNAL   Unpublished (1994)
REFERENCE   3  (sites)
  AUTHORS   Fujiwara,Y., Komiya,T., Kawabata,H., Sato,M., Fujimoto,H.,
            Furusawa,M. and Noce,T.
  TITLE     Isolation of a DEAD-family protein gene that encodes a murine
            homolog of Drosophila vasa and its specific expression in germ cell
            lineage
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 91 (25), 12258-12262 (1994)
  MEDLINE   95083681
   PUBMED   7991615
FEATURES             Location/Qualifiers
     source          1..1930
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                     /mol_type="mRNA"
                     /strain="BALB/c"
                     /sub_species="domesticus"
                     /db_xref="taxon:10090"
                     /cell_type="primordial germ cell, spermatogonium,
                     spermatocyte"
                     /tissue_type="gonad, testis"
                     /clone_lib="lambda gt10"
                     /dev_stage="adult, embryo"
     CDS             <1..1914
                     /function="RNA helicase"
                     /codon_start=1
                     /product="Drosophila vasa homologue"
                     /protein_id="BAA03584.1"
                     /db_xref="GI:286075"
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                     PAASDSGNGDTYQSRSGSGRGGYKGLNEEVVTGSGKNSWKSETEGGESSDSQGPKVTY
                     IPPPPPEDEDSIFAHYQTGINFDKYDTILVEVSGHDAPPAILTFEEANLCQTLNNNIR
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IDENTIFIERS

dbEST Id:	**1988110**
EST name:	qf47d11.x1
GenBank Acc:	AI217144
GenBank gi:	3796959

CLONE INFO

Clone Id:	IMAGE:1753173 (3')
Source:	NCI
Insert length:	1013
DNA type:	cDNA

PRIMERS

Sequencing:	-40UP from Gibco
PolyA Tail:	Unknown

SEQUENCE

TTTTTTTTTTTTTTTTTTTTTTTTGACATTTAAAATGCTTTAATATTCCCAGTTAACACC
ATTTGTATCAGTAACTGCAATGTTGTAAGTTTTAGCATCTCACATAACTAGTCAGTAAGG
ATTTTTTTTTTTAAGTGTAGGAGTGAGAATACAAGGACAGGAGCTATGAGAATGTTAAGTT
TTATACTTCTGTTAAAAACTCAAAAATCAAAACTATTTTCTTCTCTGCATCAAAACCACA
GACTTGAAGGATGTTTTGGCTTTAATCCCATGACTCATCATCTACTGGATTGGGAGCTTG
TGAAGAAGAAAACCCAGCTGTGTTCAAAGTGCTCTTGCCCTTTCTGGTATCAACTGATGC
AAACACGTTTCCTCTTGTACTACCACTGAAGCCAGGAATGTATGTACTAAAGGCAATTTC
TTCCAACCATGCAGGAACATCCTGTTGAGCATCTGTCAATACTTTTACTAGAGGCTGTGC
TAAATGGTTATCCGATTCAAGATCAAAAAAGGAAATTGCTCTGCCAGTATTCCCACAACG
ACCAGNACGCCCAAT

Quality: High quality sequence stops at base: 448

Entry Created:	Oct 26 1998
Last Updated:	Nov 10 1998

COMMENTS

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

PUTATIVE ID Assigned by submitter
SW:DDX4_RAT Q64060 DEAD BOX PROTEIN 4 ;

LIBRARY

Lib Name:	Soares_testis_NHT
Organism:	Homo sapiens
Sex:	male
Lab host:	DH10B
Vector:	pT7T3D-Pac (Pharmacia) with a modified polylinker

?. Site 1:	Not I
?. Site 2:	Eco RI
Description:	1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo (dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCCCAATTTTTTTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo.

SUBMITTER

Name:	Robert Strausberg, Ph.D.
E-mail:	cgapbs-r@mail.nih.gov

CITATIONS

Title:	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Authors:	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
Year:	1997
Status:	Unpublished

MAP DATA

1: AI953070. wq49h07.x1 NCI_CG...[gi:5745380] Links

IDENTIFIERS

dbEST Id:	**3076455**
EST name:	wq49h07.x1
GenBank Acc:	AI953070
GenBank gi:	5745380

CLONE INFO

Clone Id:	IMAGE:2474653 (3')
Source:	NCI
Insert length:	450
DNA type:	cDNA

PRIMERS

Sequencing:	-40UP from Gibco
PolyA Tail:	Unknown

SEQUENCE

TTTTTTTTTTATGAGAATGTTAAGTTTTATACTTCTGTTAAAAACTCAAAAATCAAAACT
ATTTTCTTCTCTGCATCAAAACCACAGACTTGAAGGATGTTTTGGCTTTAATCCCATGAC
TCATCATCTACTGGATTGGGAGCTTGTGAAGAAGAAAACCCAGCTGTGTTCAAAGTGCTC
TTGCCCTTTCTGGTATCAACTGATGCAAACACGTTTCCTCTTGTACTACCACTGAAGCCA
GGAATGTATGTACTAAAGGCAATTTCTTCCAACCATGCAGGAACATCCTGTTGAGCATCT
GTCAATACTTTTACTAGAGGCTGTGCTAAATGGTTATCCGATTCAAG

Entry Created:	Aug 19 1999
Last Updated:	Mar 8 2000

COMMENTS

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

PUTATIVE ID	Assigned by submitter SW:DDX4_RAT Q64060 DEAD BOX PROTEIN 4 ;

LIBRARY

Lib Name:	NCI_CGAP_GC6
Organism:	Homo sapiens
Tissue type:	pooled germ cell tumors
Lab host:	DH10B
Vector:	pT7T3D-Pac (Pharmacia) with a modified polylinker
R. Site 1:	Not I
R. Site 2:	Eco RI
Description:	Plasmid DNA from the normalized library NCI_CGAP_GC4 was

prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo.

SUBMITTER

Name: Robert Strausberg, Ph.D.
E-mail: cgapbs-r@mail.nih.gov

CITATIONS

Title: National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Authors: NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
Year: 1997
Status: Unpublished

MAP DATA

37

1: AI025074. ov40a04.x1 Soares...[gi:3240687]

IDENTIFIERS

dbEST Id:	**1764280**
EST name:	ov40a04.x1
GenBank Acc:	AI025074
GenBank gi:	3240687

CLONE INFO

Clone Id:	IMAGE:1639758 (3')
Source:	NCI
Insert length:	587
DNA type:	cDNA

PRIMERS

Sequencing:	-40m13 fwd. ET from Amersham
PolyA Tail:	Unknown

SEQUENCE

TTTTGACATTTAGAATGCTTTAATATTCCCAGTTAACACCATTTGTATCAGTAACTGCAA
TGTTGTAAGTTTTAGCATCTCACATAACTAGTCAGTAAGGATTTTTTTTTTAAGTGTAGG
AGTGAGAATACAAGGACAGGAGCTATGAGAATGTTAAGTTTTATACTTCTGTTAAAAACT
CAAAAATCAAAACTATTTTCTTCTCTGCATCAAAACCACAGACTTGAAGGATGTTTTGGC
TTTAATCCCATGACTCATCATCTACTGGATTGGGAGCTTGTGAAGAAGAAAACCCAGCTG
TGTTCAAAGTGCTCTTGCCCTTTCTGGATCAACTGATGCANAACCGTTTCCTCTTGTACT
ACCACTGAAGCCAGGAATGTTGTACTAAAGGCAATTTCTTCCAACCATGCAGGAACATCC
TGTTGAGCATCTGTCAATACTTTACTAGAAGCTGTGCTAAATGGTTATC

Quality:	High quality sequence stops at base: 408
Entry Created:	Aug 13 1998
Last Updated:	Aug 27 1998

COMMENTS

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

PUTATIVE ID	Assigned by submitter SW:DDX4_RAT Q64060 DEAD BOX PROTEIN 4 ;

LIBRARY

Lib Name:	Soares_testis_NHT
Organism:	Homo sapiens
Sex:	male
Lab host:	DH10B
Vector:	pT7T3D-Pac (Pharmacia) with a modified polylinker
R. Site 1:	Not I
R. Site 2:	Eco RI

Description: 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo (dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCCCAATTTTTTTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo.

SUBMITTER

Name: Robert Strausberg, Ph.D.
E-mail: cgapbs-r@mail.nih.gov

CITATIONS

Title: National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Authors: NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
Year: 1997
Status: Unpublished

MAP DATA

NCBI

Sequence Revision History

Revision history for AI953070

GI	Version	Update Date	Status
5745380	1	Aug 19 1999 7:22 PM	Live

Accession AI953070 was first seen at NCBI on Aug 19 1999 7:22 PM

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38

1: AI654417. wb31f04.x1 NCI_CG...[gi:4738396] Links

IDENTIFIERS

dbEST Id: **2483061**
EST name: wb31f04.x1
GenBank Acc: AI654417
GenBank gi: 4738396

CLONE INFO
Clone Id: IMAGE:2307295 (3')
Source: NCI
Insert length: 376
DNA type: cDNA

PRIMERS
Sequencing: -40UP from Gibco
PolyA Tail: Unknown

SEQUENCE

AAGTGTAGGTTTGAGAATACAAGGACAGGAGCTATGAGAATGTTAAGTTTTATACTTCTG
TTAAAAACTCAAAAATCAAAACTATTTTCTTCTCTGCATCAAAACCACAGACTTGAAGGA
TGTTTTGGCTTTAATCCCATGACTCATCATCTACTGGATTGGGAGCTTGTGAAGAAGAAA
ACCCAGCTGTGTTCAAAGTGCTCTTGCCCTTTCTGGTATCAACTGATGCAAACACGTTTC
CTCTTGTACTACCACTGAAGCCAGGAATGTATGTACTAAAGGCAATTTCTTCCAACCATG

Entry Created: May 4 1999
Last Updated: Dec 17 1999

COMMENTS

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

PUTATIVE ID Assigned by submitter
SW:DDX4_RAT Q64060 DEAD BOX PROTEIN 4 ;

LIBRARY
Lib Name: NCI_CGAP_GC6
Organism: Homo sapiens
Tissue type: pooled germ cell tumors
Lab host: DH10B
Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker
R. Site 1: Not I
R. Site 2: Eco RI
Description: Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP

purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo.

SUBMITTER

Name: Robert Strausberg, Ph.D.
E-mail: cgapbs-r@mail.nih.gov

CITATIONS

Title: National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Authors: NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
Year: 1997
Status: Unpublished

MAP DATA

NCBI

Sequence Revision History

Revision history for AI654417

GI	Version	Update Date	Status
4738396	1	May 4 1999 7:20 PM	Live

Accession AI654417 was first seen at NCBI on May 4 1999 7:20 PM

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1: AI337133. qx83b04.x1 NCI_CG...[gi:4074060] Links

IDENTIFIERS

dbEST Id:	**2120875**
EST name:	qx83b04.x1
GenBank Acc:	AI337133
GenBank gi:	4074060

CLONE INFO

Clone Id:	IMAGE:2009071 (3')
Source:	NCI
DNA type:	cDNA

PRIMERS

Sequencing:	-40UP from Gibco
PolyA Tail:	Unknown

SEQUENCE

AAGTGTAGGAGTGAGAATACAAGGACAGGAGCTATGAGAATGTTAAGTTTTATACTTCTG
TTAAAAACTCAAAAATCAAAACTATTTTCTTCTCTGCATCAAAACCACAGACTTGAAGGA
TGTTTTGGCTTTAATCCCATGACTCATCATCTACTGGATTGGGAGCTTGTGAAGAAGAAA
ACCCAGCTGTGTTCAAAGTGCTCTTGCCCTTTCTGGTATCAACTGATGCAAACACGTTTC
CTCTTGTACTACCACTGAAGCCAGGAATGTATGTACTAAAGGCAATTTCTTCCAACCATG

Entry Created:	Dec 29 1998
Last Updated:	Dec 29 1998

COMMENTS

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

PUTATIVE ID	Assigned by submitter SW:DDX4_RAT Q64060 DEAD BOX PROTEIN 4 ;

LIBRARY

Lib Name:	NCI_CGAP_GC6
Organism:	Homo sapiens
Tissue type:	pooled germ cell tumors
Lab host:	DH10B
Vector:	pT7T3D-Pac (Pharmacia) with a modified polylinker
R. Site 1:	Not I
R. Site 2:	Eco RI
Description:	Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive

hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo.

SUBMITTER

Name: Robert Strausberg, Ph.D.
E-mail: cgapbs-r@mail.nih.gov

CITATIONS

Title: National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Authors: NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
Year: 1997
Status: Unpublished

MAP DATA

1: AA758412. ah66g05.s1 Soares...[gi:2806275] Links

IDENTIFIERS

dbEST Id:	**1480155**
EST name:	ah66g05.s1
GenBank Acc:	AA758412
GenBank gi:	2806275

CLONE INFO

Clone Id:	1320632 (3')
Source:	IMAGE Consortium, LLNL
Insert length:	416
DNA type:	cDNA

PRIMERS

Sequencing:	-40m13 fwd. ET from Amersham
PolyA Tail:	Unknown

SEQUENCE

TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGACATTTAGAATGCTTTAATATTCCCAG
TTAACACCATTTGTATCAGTAACTGCAATGTTGTAAGTTTTAGCATCTCACATAACTAGT
CAGTAAGGATTTTTTTTTTAAGTGTAGGAGTGAGAATACAAGGACAGGAGCTATGAGAAT
GTTAAGTTTTATACTTCTGTTAAAAACTCAAAAATCAAAACTATTTTCTTCTCTGCATCA
AAACCACAGACTTGAAGGATGTTTTGGCTTTAATCCCATGACTCATCATCTACTGGATTG
GGAGCTTGTGAAGAAGAAAACCCAGCTGTGTTCAAAGTGCTCTTGCCCTTTCTGGTATCA
ACTGATGCAAA

Quality: High quality sequence stops at base: 206

Entry Created:	Jan 23 1998
Last Updated:	Dec 29 1998

COMMENTS

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Possible reversed clone: similarity on wrong strand

PUTATIVE ID	Assigned by submitter
	SW:DDX4_RAT Q64060 DEAD BOX PROTEIN 4 ;

LIBRARY

Lib Name:	Soares_testis_NHT
Organism:	Homo sapiens
Sex:	male
Lab host:	DH10B
Vector:	pT7T3D-Pac (Pharmacia) with a modified polylinker
R. Site 1:	Not I
R. Site 2:	Eco RI

Description: 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo (dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCCCAATTTTTTTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo.

SUBMITTER

Name: Robert Strausberg, Ph.D.
E-mail: cgapbs-r@mail.nih.gov

CITATIONS

Title: National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Authors: NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
Year: 1997
Status: Unpublished

MAP DATA

41

1: AI969018. wq68d02.x1 NCI_CG...[gi:5765757]

IDENTIFIERS

dbEST Id:	**3095021**
EST name:	wq68d02.x1
GenBank Acc:	AI969018
GenBank gi:	5765757

CLONE INFO

Clone Id:	IMAGE:2476419 (3')
Source:	NCI
Insert length:	429
DNA type:	cDNA

PRIMERS

Sequencing:	-40UP from Gibco
PolyA Tail:	Unknown

SEQUENCE

GAATGTATGTACTAAAGGCAATTTCTTCCAACCATGCAGGAACATCCTGTTGAGCATCTG
TCAATACTTTTACTAGAGGCTGTGCTAAATGGTTATCCGATTCAAGAT

Quality: Trace considered overall poor quality.

Entry Created:	Aug 25 1999
Last Updated:	Oct 20 2000

COMMENTS

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality

PUTATIVE ID Assigned by submitter
SW:DDX4_RAT Q64060 DEAD BOX PROTEIN 4 ;

LIBRARY

Lib Name:	NCI_CGAP_GC6
Organism:	Homo sapiens
Tissue type:	pooled germ cell tumors
Lab host:	DH10B
Vector:	pT7T3D-Pac (Pharmacia) with a modified polylinker
R. Site 1:	Not I
R. Site 2:	Eco RI
Description:	Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive

hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo.

SUBMITTER

Name: Robert Strausberg, Ph.D.
E-mail: cgapbs-r@mail.nih.gov

CITATIONS

Title: National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Authors: NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
Year: 1997
Status: Unpublished

MAP DATA

NCBI

Sequence Revision History

Revision history for AI969018

GI	Version	Update Date	Status
5765757	1	Aug 25 1999 7:04 PM	Live

Accession AI969018 was first seen at NCBI on Aug 25 1999 7:04 PM

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LocusLink provides curated information for human, fruit fly, mouse, rat, and zebrafish

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1: AA400066. zu62a08.s1 Soares...[gi:2053869] Links

IDENTIFIERS

dbEST Id:	**1041638**
EST name:	zu62a08.s1
GenBank Acc:	AA400066
GenBank gi:	2053869
GDB Id:	5929433

CLONE INFO

Clone Id:	IMAGE:742550 (3')
Source:	IMAGE Consortium, LLNL
Insert length:	521
DNA type:	cDNA

PRIMERS

Sequencing:	-41m13 fwd. ET from Amersham
PolyA Tail:	Unknown

SEQUENCE

GAATGTATGTACTATAGGCAATTTCTTCCATCCATGTCGGAACATCCTGTTGAGCATCTG
TCAATACTTTTACTAGAGGCTGTGCTACATGGCTAACCGAATC

Quality: Trace considered overall poor quality.

Entry Created: Dec 20 1996
Last Updated: Nov 9 1997

COMMENTS

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand

PUTATIVE ID Assigned by submitter
TR:G806464 G806464 VASA-LIKE GENE PROTEIN. ;

LIBRARY

Lib Name:	Soares_testis_NHT
Organism:	Homo sapiens
Sex:	male
Lab host:	DH10B
Vector:	pT7T3D-Pac (Pharmacia) with a modified polylinker
R. Site 1:	Not I
R. Site 2:	Eco RI
Description:	1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo (dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCCCAATTTTTTTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo.

SUBMITTER

Name: Wilson RK
Institution: Washington University School of Medicine
Address: 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
E-mail: est@watson.wustl.edu

CITATIONS

Title: WashU-NCI human EST Project
Authors: Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost ,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra ,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan ,F., Theising,B., White,Y., Wylie,T., Waterston,R., Wilson ,R.
Year: 1997
Status: Unpublished

MAP DATA

A13

1: AA862553. oh44b08.s1 NCI_CG...[gi:2955032] Links

IDENTIFIERS

dbEST Id: **1588408**
EST name: oh44b08.s1
GenBank Acc: AA862553
GenBank gi: 2955032

CLONE INFO
Clone Id: IMAGE:1469463 (3')
Source: NCI
Insert length: 1202
DNA type: cDNA

PRIMERS
Sequencing: -40m13 fwd. ET from Amersham
PolyA Tail: Unknown

SEQUENCE

GAATGTATGTACTAAAGGCAATTTCTTCCAACCATGCAGTGACATCATGTTGAGCATCTG
TCAATACTTTTACTAGATGCTGTCTATAATAGGTATCGGA
Quality: Trace considered overall poor quality.

Entry Created: Mar 4 1998
Last Updated: Aug 24 1998

COMMENTS

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D.,
Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing
Center
Clone distribution: NCI-CGAP clone distribution information
can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality

PUTATIVE ID Assigned by submitter
SW:DDX4_RAT Q64060 DEAD BOX PROTEIN 4 ;

LIBRARY
Lib Name: NCI_CGAP_GC4
Organism: Homo sapiens
Tissue type: pooled germ cell tumors
Lab host: DH10B
Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker
Description: 1st strand cDNA was prepared from 3 pooled germ cell tumors,
and was then primed with a Not I - oligo(dT) primer.
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library is
normalized. Library was constructed by Bento Soares and M.

Fatima Bonaldo.

SUBMITTER

Name: Robert Strausberg, Ph.D.
E-mail: cgapbs-r@mail.nih.gov

CITATIONS

Title: National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Authors: NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
Year: 1997
Status: Unpublished

MAP DATA

1: AA401568. zu62a08.r1 Soares...[gi:2053983] Links

IDENTIFIERS

dbEST Id:	**1041752**
EST name:	zu62a08.r1
GenBank Acc:	AA401568
GenBank gi:	2053983
GDB Id:	5929433

CLONE INFO

Clone Id:	IMAGE:742550 (5')
Source:	IMAGE Consortium, LLNL
Insert length:	521
DNA type:	cDNA

PRIMERS

Sequencing:	-28m13 rev2 ET from Amersham
PolyA Tail:	Unknown

SEQUENCE

TTCTACCATTGATGAATATGTTCATCGACTTGGGCGTACTGGTCGTTGTGGGAATACTGG
CAGAGCAAGTTTCCTTTTT

Quality: Trace considered overall poor quality.

Entry Created:	Dec 20 1996
Last Updated:	Nov 9 1997

COMMENTS

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand

PUTATIVE ID Assigned by submitter
TR:G286075 G286075 DROSOPHILA VASA HOMOLOGUE ;

LIBRARY

Lib Name:	Soares_testis_NHT
Organism:	Homo sapiens
Sex:	male
Lab host:	DH10B
Vector:	pT7T3D-Pac (Pharmacia) with a modified polylinker
R. Site 1:	Not I
R. Site 2:	Eco RI
Description:	1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo (dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCCCAATTTTTTTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was

constructed by Bento Soares and M. Fatima Bonaldo.

SUBMITTER

Name: Wilson RK
Institution: Washington University School of Medicine
Address: 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
E-mail: est@watson.wustl.edu

CITATIONS

Title: WashU-NCI human EST Project
Authors: Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost ,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra ,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan ,F., Theising,B., White,Y., Wylie,T., Waterston,R., Wilson ,R.
Year: 1997
Status: Unpublished

MAP DATA

1: AA316798. EST188483 HCC cel...[gi:1969147] Links

IDENTIFIERS

dbEST Id: 958127
EST name: EST188483
GenBank Acc: AA316798
GenBank gi: 1969147

CLONE INFO
Clone Id: (5' end)
Source: ATCC
Id in host: 113555
Other ESTs on clone: THC127206
DNA type: cDNA

PRIMERS
Sequencing: M13 Reverse
PolyA Tail: Unknown

SEQUENCE

GAAAGATTGGATTAGACTTTTGCAAATACTTGGTGTTAGATGAAGCTGATCGGATGTTGG
ATATGGGGTTTGAGCCTCAGATTCGTAGAATAGTCGAACAAGATACTATGCCTCCAAAGG
GTGTCCGCCACACTATGATGTTTAGTGCTACTTTTCCTAAGGAAATACAGATGCTGGCTC
GTGATTTCTTAGATGAATATATCTTCTTGGCTGTAGGAAGAGTTGGCTCTACCTCTGAAA
ACATCACACAGAAAGTAGTTTGGGTGGAAGAATCAGACAAACGGTCATTTCTGCTTGACC
TCCTAAATGCAACAGGCAAGGATTCACTGACCTTAGTGTTTGTGGAGACCAAAAAGGGTG
CAGATTCTCTGGAGGATTTCTTATACCATGAAGGATACGCATGTACCAGCATCCATGGAG
ACCGTTCTCAGAGGGATAGAGAAGAGGCCCTTCAACAGTTCCGCTCAGGGA

Entry Created: Apr 19 1997
Last Updated: Apr 19 1997

COMMENTS

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)

PUTATIVE ID Assigned by submitter
similar to RNA helicase

LIBRARY
Lib Name: HCC cell line (matastasis to liver in mouse) II
Organism: Homo sapiens
Tissue type: colon
Cell type: KM12SM
Cell line: KM12C(HCC)metastasis into mouse (liver)
Vector: pBluescript SK-
R. Site 1: EcoRI
R. Site 2: XhoI

SUBMITTER
Name: Kerlavage, AR
Lab: Bioinformatics

Institution: The Institute for Genomic Research
Address: 9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
E-mail: arkerlav@tigr.org

CITATIONS

Medline UID: 96026280
Title: Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Authors: Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M., Venter,J.C.
Citation: Nature 377 (6547 Suppl): 3-174 1995

MAP DATA

1: T85890. yd58g05.r1 Soares...[gi:714242] Links

IDENTIFIERS

dbEST Id:	**156011**
EST name:	yd58g05.r1
GenBank Acc:	T85890
GenBank gi:	714242
GDB Id:	468089

CLONE INFO

Clone Id:	IMAGE:112472 (5')
Insert length:	1604
DNA type:	cDNA

PRIMERS

Sequencing:	M13RP1
PolyA Tail:	Unknown

SEQUENCE

TTTTGCAAATACTTGGTGTTAGATGAAGCTGATCGGATGTTGGATATGGGGTTTGAGCCT
CAGATTCGTAGAATAGTCGAACAAGATACTATGCCTCCAAAGGGTGTCCGCCACACTATG
ATGTTTAGTGCTACTTTTCCTAAGGAAATACAGATGCTGGCTCGTGATTTCTTAGGATGA
ATATATCTTCTTGGGCTGTAGGGAAGGAGTTGGGCTCTACCTCTGGAAAACATCACACAG
GAAAGTAGTTGGGGTGGGAAGGANTCAGGACAAACGGGTCATTTCTGGCTTGACCCTCCC
TAAATGGCAACAGGGGCAAGGGATTTCACTTGACCNTTAGGTGTTTTGTGGGGGAGACCC
CAAAAGGGGGTGCCAGGNTTC

Quality: High quality sequence stops at base: 281

Entry Created:	Mar 17 1995
Last Updated:	Mar 17 1995

COMMENTS

Insert Size: 1604
High quality sequence stops: 281 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

PUTATIVE ID Assigned by submitter
SP:PL10_MOUSE P16381 PUTATIVE ATP-DEPENDENT RNA HELICASE ;

LIBRARY

Lib Name:	Soares fetal liver spleen 1NFLS
Organism:	Homo sapiens
Sex:	male
Organ:	Liver and Spleen
Develop. stage:	20 week-post conception fetus
Lab host:	DH10B (ampicillin resistant)
Vector:	pT7T3D (Pharmacia) with a modified polylinker
R. Site 1:	Pac I
R. Site 2:	Eco RI
Description:	1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

SUBMITTER

Name:	Wilson RK
Institution:	Washington University School of Medicine
Address:	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel:	314 286 1800
Fax:	314 286 1810
E-mail:	est@watson.wustl.edu

CITATIONS

Title:	The WashU-Merck EST Project
Authors:	Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M. , Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P., Wilson,R.
Year:	1995
Status:	Unpublished

MAP DATA

47

1: T82153. yd95d08.r1 Soares...[gi:705160] Links

IDENTIFIERS

dbEST Id:	**147970**
EST name:	yd95d08.r1
GenBank Acc:	T82153
GenBank gi:	705160
GDB Id:	471600

CLONE INFO

Clone Id:	IMAGE:115983 (5')
Other ESTs on clone:	yd95d08.s1
Insert length:	860
DNA type:	cDNA

PRIMERS

Sequencing:	M13RP1
PolyA Tail:	Unknown

SEQUENCE

TTTTGCAAATACTTGGTGTTAGATGAAGCTGATCGGATGTTGGATATGGGGTTTGAGCCT
CAGATTCGTAGAATAGTCGAACAAGATACTATGCCTCCAAAGGGTGTCCGCCACACTATG
ATGTTTAGTGCTACTTTTCCTAAGGAAATACAGATGCTGGCTCGTGATTTCTTAGATGAA
TATATCTTCTTGGGCTGTAGGGAAGAGTTGGCTCTACCTCTGAAAACATCACACAGAAAG
TAGTTGGGGTGGGAAGGAATCAGACAAACGGTCATTTCTGGCTTGGACCTCCTAAATGGC
AACAGGGCAAGGGTTCACTTGACCTTAGTGTTTTGTTGGGAGACCCAAAAAGGGGTGCCA
G

Quality: High quality sequence stops at base: 269

Entry Created: Mar 10 1995
Last Updated: Mar 15 1995

COMMENTS

Insert Size: 860
High quality sequence stops: 269 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

PUTATIVE ID Assigned by submitter
SP:PL10_MOUSE P16381 PUTATIVE ATP-DEPENDENT RNA HELICASE ;

LIBRARY

Lib Name:	Soares fetal liver spleen 1NFLS
Organism:	Homo sapiens
Sex:	male
Organ:	Liver and Spleen
Develop. stage:	20 week-post conception fetus
Lab host:	DH10B (ampicillin resistant)
Vector:	pT7T3D (Pharmacia) with a modified polylinker
R. Site 1:	Pac I
R. Site 2:	Eco RI
Description:	1st strand cDNA was primed with a Pac I - oligo(dT) primer

[5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

SUBMITTER

Name:	Wilson RK
Institution:	Washington University School of Medicine
Address:	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel:	314 286 1800
Fax:	314 286 1810
E-mail:	est@watson.wustl.edu

CITATIONS

Title:	The WashU-Merck EST Project
Authors:	Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M. , Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P., Wilson,R.
Year:	1995
Status:	Unpublished

MAP DATA
